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WHAT IS CLAIMED IS:

1. A method of identifying putative naturally occurring antisense transcripts, the method comprising:

(a) computationally aligning a first database including sense-oriented polynucleotide sequences with a second database including expressed polynucleotide sequences; and

(b) identifying expressed polynucleotide sequences from said second database being capable of forming a duplex with at least one sense-oriented polynucleotide sequence of said first database, thereby identifying putative naturally occurring antisense transcripts.

2. The method of claim 1, wherein said first database includes sequences of a type selected from the group consisting of genomic sequences, expressed sequence tags, contigs, intron sequences, complementary DNA (cDNA) sequences, pre-messenger RNA (mRNA) sequences and mRNA sequences.

3. The method of claim 1, wherein said second database includes sequences of a type selected from the group consisting of expressed sequence tags, contigs, complementary DNA (cDNA) sequences, pre-messenger RNA (mRNA) sequences and mRNA sequences.

4. The method of claim 1, wherein an average sequence length of said expressed polynucleotide sequences of said second database is selected from a range of 0.02 to 0.8 Kb.

5. The method of claim 1, wherein said second database is generated by:

(i) providing a library of expressed polynucleotides;

(ii) obtaining sequence information of said expressed polynucleotides;

(iii) computationally selecting at least a portion of said expressed polynucleotides according to at least one sequence criterion; and

(iv) storing said sequence information of said at least a portion of said expressed polynucleotides thereby generating said second database.

6. The method of claim 5, wherein said at least one sequence criterion for computationally selecting said at least a portion of said expressed polynucleotide is selected from the group consisting of sequence length, sequence annotation, sequence information, intron splice consensus site, intron sharing, sequence overlap, rare restriction site, poly(T) head, poly(A) tail, and poly(A) signal.

7. The method of claim 1 further comprising the step of testing the putative naturally occurring antisense transcripts for an ability to form said duplex with said at least one sense oriented polynucleotide sequence under physiological conditions.

8. The method of claim 1 further comprising the step of computationally testing the putative naturally occurring antisense transcripts according to at least one criterion selected from the group consisting of sequence annotation, sequence information, intron splice consensus site, intron sharing, sequence overlap, rare restriction site, poly(T) head, poly(A) tail, and poly(A) signal.

9. A kit for quantifying at least one mRNA transcript of interest, the kit comprising at least one oligonucleotide being designed and configured so as to be complementary to a sequence region of the mRNA transcript of interest, said sequence region not being complementary with a naturally occurring antisense transcript.

10. The kit of claim 9, wherein a length of said at least one oligonucleotide is selected from a range of 15-200 nucleotides.

11. The kit of claim 9, wherein said at least one oligonucleotide is a single stranded oligonucleotide.

12. The kit of claim 9, wherein said at least one oligonucleotide is a double stranded oligonucleotide.

13. The kit of claim 9, wherein a guanidine and cytosine content of said at least one oligonucleotide is at least 25 %.

14. The kit of claim 9, wherein said at least one oligonucleotide is labeled.

15. The kit of claim 9, wherein said at least one oligonucleotide is attached to a solid substrate.

16. The kit of claim 15, wherein said solid substrate is configured as a microarray and whereas said at least one oligonucleotide includes a plurality of oligonucleotides each attached to said microarray in a regio-specific manner.

17. A kit for quantifying at least one mRNA transcript of interest, the kit comprising at least one pair of oligonucleotides including a first oligonucleotide capable of binding the at least one mRNA transcript of interest and a second oligonucleotide being capable of binding a naturally occurring antisense transcript complementary to the mRNA of interest.

18. The kit of claim 17, wherein a length of each of said first and second oligonucleotides is selected from a range of 15-200 nucleotides

19. The kit of claim 17, wherein said first and second oligonucleotides are single stranded oligonucleotides.

20. The kit of claim 17, wherein said first and second oligonucleotides are double stranded oligonucleotide.

21. The kit of claim 17, wherein a guanidine and cytosine content of each of said first and second oligonucleotides is at least 25 %.

22. The kit of claim 17, wherein said first and second oligonucleotides are labeled.

23. The kit of claim 17, wherein said first and second oligonucleotides are attached to a solid substrate.

24. The kit of claim 23, wherein said solid substrate is configured as a microarray and whereas each of said first and second oligonucleotides includes a plurality of oligonucleotides each attached to said microarray in a regio-specific manner.

25. A kit for quantifying at least one naturally occurring antisense transcript of interest, the kit comprising at least one oligonucleotide being designed and configured so as to be complementary to a sequence region of the at least one naturally occurring antisense transcript of interest, said sequence region not being complementary with a naturally occurring mRNA transcript.

26. The kit of claim 25, wherein a length of said at least one oligonucleotide is selected from a range of 15-200 nucleotides.

27. The kit of claim 25, wherein said at least one oligonucleotide is a single stranded oligonucleotide.

28. The kit of claim 25, wherein said at least one oligonucleotide is a double stranded oligonucleotide.

29. The kit of claim 25, wherein a guanidine and cytosine content of said at least one oligonucleotide is at least 25 %.

30. The kit of claim 25, wherein said at least one oligonucleotide is labeled.

31. The kit of claim 25, wherein said at least one oligonucleotide is attached to a solid substrate.

32. The kit of claim 31, wherein said solid substrate is configured as a microarray and whereas said at least one oligonucleotide includes a plurality of oligonucleotides each attached to said microarray in a regio-specific manner.

33. A method of designing artificial antisense transcripts, the method comprising:

(a) providing a database of naturally occurring antisense transcripts;

(b) extracting from said database criteria governing structure and/or function of said naturally occurring antisense transcripts; and

(c) designing the artificial antisense transcripts according to said criteria.

34. The method of claim 33, wherein said criteria governing structure and/or function of said naturally occurring antisense transcripts are selected from the group consisting of antisense length, complementarity length, complementarity position, intron molecules, alternative splicing sites, tissue specificity, pathological abundance, chromosomal mapping, open reading frames, promoters, hairpin structures, helix structures, stem and loops, pseudoknots and tertiary interactions, guanidine and/or cytosine content, guanidine tandems, adenosine content, thermodynamic criteria, RNA duplex melting point, RNA modifications, protein-binding motifs, palindromic sequence and predicted single stranded and double stranded regions.

35. The method of claim 33, wherein said step of providing said database of naturally occurring antisense transcripts is effected by:

(a) computationally aligning a first database including sense-oriented polynucleotide sequences with a second database including expressed polynucleotide sequences; and

(b) identifying expressed polynucleotide sequences from said second database being capable of forming a duplex with at least one sense-oriented polynucleotide sequence of said first database,

(c) storing a sequence of said expressed polynucleotide sequences identified in step (b), thereby providing said database of said naturally occurring antisense transcripts..

36. The method of claim 35, wherein said first database includes sequences of a type selected from the group consisting of genomic sequences, expressed sequence tags, contigs, intron sequences, complementary DNA (cDNA) sequences, pre-messenger RNA (mRNA) sequences and mRNA sequences.

37. The method of claim 35, wherein said second database includes sequences of a type selected from the group consisting of expressed sequence tags, contigs, complementary DNA (cDNA) sequences, pre-messenger RNA (mRNA) sequences and mRNA sequences.

38. The method of claim 35, wherein an average sequence length of said expressed polynucleotide sequences of said second database is selected from a range of 0.02 to 0.8 Kb.

39. The method of claim 35, wherein said second database is generated by:

(i) providing a library of expressed polynucleotides;

(ii) obtaining sequence information of said expressed polynucleotides;

(iii) computationally selecting at least a portion of said expressed polynucleotides according to at least one sequence criterion; and

(iv) storing said sequence information of said at least a portion of said expressed polynucleotides thereby generating said second database.

40. The method of claim 39, wherein said at least one sequence criterion for computationally selecting said at least a portion of said expressed polynucleotide is selected from the group consisting of sequence length, sequence annotation,

sequence information, intron splice consensus site, intron sharing, sequence overlap, rare restriction site , poly(T) head, poly(A) tail, and poly(A) signal.

41. The method of claim 35, further comprising the step of testing said putative naturally occurring antisense transcripts for an ability to form said duplex with said at least one sense oriented polynucleotide sequence under physiological conditions.

42. The method of claim 35 further comprising the step of computationally testing said putative naturally occurring antisense transcripts according to at least one criterion selected from the group consisting of sequence annotation, sequence information, intron splice consensus site, intron sharing, sequence overlap, rare restriction site , poly(T) head, poly(A) tail, and poly(A) signal.

43. A computer readable storage medium comprising a database including a plurality of sequences, wherein each sequence is of a naturally occurring antisense transcript.

44. The computer readable storage medium of claim 43, wherein said database further includes information pertaining to each sequence of said naturally occurring antisense transcripts, said information is selected from the group consisting of related sense gene, antisense length, complementarity length, complementarity position, intron molecules, alternative splicing sites, tissue specificity, pathological abundance, chromosomal mapping, open reading frames, promoters, hairpin structures, helix structures, stem and loops, pseudoknots and tertiary interactions, guanidine and/or cytosine content, guanidine tandems, adenosine content, thermodynamic criteria, RNA duplex melting point, RNA modifications, protein-binding motifs, palindromic sequence and predicted single stranded and double stranded regions.

45. The computer readable storage medium of claim 43, wherein said database further includes information pertaining to generation of said database and potential uses of said database.

46. A method of generating a database of naturally occurring antisense transcripts, the method comprising:

(a) computationally aligning a first database including sense-oriented polynucleotide sequences with a second database including expressed polynucleotide sequences;

(b) identifying expressed polynucleotide sequences from said second database being capable of forming a duplex with at least one sense-oriented polynucleotide sequence of said first database so as to identify putative naturally occurring antisense transcripts; and

(c) storing sequence information of said identified naturally occurring antisense transcripts, thereby generating the database of the naturally occurring antisense transcripts.

47. The method of claim 46, wherein the database is set forth in the file seqs_125 and/or seqs_133 of the enclosed CD-ROM1, alignments_125, table_125, Table_S1 and/or Table_S2 of the enclosed CD-ROM2, alignments_133 and/or table_133 of the enclosed CD-ROM3, alignments_136, mouse_alignments, mouse_seqs, mouse_table, nuc_seqs_136, orthology, pep_seqs_136, table_136, annotations_136 and/or antisense of the enclosed CD-ROM4.

48. The method of claim 46, wherein said first database includes sequences of a type selected from the group consisting of genomic sequences, expressed sequence tags, contigs, intron sequences, complementary DNA (cDNA) sequences, pre-messenger RNA (mRNA) sequences and mRNA sequences.

49. The method of claim 46, wherein said second database includes sequences of a type selected from the group consisting of expressed sequence tags,

contigs, complementary DNA (cDNA) sequences, pre-messenger RNA (mRNA) sequences and mRNA sequences.

50. The method of claim 46, wherein an average sequence length of said expressed polynucleotide sequences of said second database is selected from a range of 0.02 to 0.8 Kb.

51. The method of claim 46, wherein said second database is generated by:

(i) providing a library of expressed polynucleotides;

(ii) obtaining sequence information of said expressed polynucleotides;

(iii) computationally selecting at least a portion of said expressed polynucleotides according to at least one sequence criterion; and

(iv) storing said sequence information of said at least a portion of said expressed polynucleotides thereby generating said second database.

52. The method of claim 51, wherein said at least one sequence criterion for computationally selecting said at least a portion of said expressed polynucleotide is selected from the group consisting of sequence length, sequence annotation, sequence information, intron splice consensus site, intron sharing, sequence overlap, rare restriction site , poly(T) head, poly(A) tail, and poly(A) signal.

53. The method of claim 46 further comprising the step of testing the putative naturally occurring antisense transcripts for an ability to form said duplex with said at least one sense oriented polynucleotide sequence under physiological conditions.

54. The method of claim 46 further comprising the step of computationally testing the putative naturally occurring antisense transcripts according to at least one criterion selected from the group consisting of sequence annotation, sequence information, intron splice consensus site, intron sharing, sequence overlap, rare restriction site , poly(T) head, poly(A) tail, and poly(A) signal.

55. A system for generating a database of a plurality of putative naturally occurring antisense transcripts, the system comprising a processing unit, said processing unit executing a software application configured for:

(a) computationally aligning a first database including sense-oriented polynucleotide sequences with a second database including expressed polynucleotide sequences; and

(b) identifying expressed polynucleotide sequences from said second database being capable of forming a duplex with at least one sense-oriented polynucleotide sequence of said first database.

56. The system of claim 55, wherein said first database includes sequences of a type selected from the group consisting of genomic sequences, expressed sequence tags, contigs, intron sequences, complementary DNA (cDNA) sequences, pre-messenger RNA (mRNA) sequences and mRNA sequences.

57. The system of claim 55, wherein said second database includes sequences of a type selected from the group consisting of expressed sequence tags, contigs, complementary DNA (cDNA) sequences, pre-messenger RNA (mRNA) sequences and mRNA sequences.

58. The system of claim 55, wherein an average sequence length of said expressed polynucleotide sequences of said second database is selected from a range of 0.02 to 0.8 Kb.

59. The system of claim 55, wherein said second database is generated by:

(i) providing a library of expressed polynucleotides;

(ii) obtaining sequence information of said expressed polynucleotides;

(iii) computationally selecting at least a portion of said expressed polynucleotides according to at least one sequence criterion; and

(iv) storing said sequence information of said at least a portion of said expressed polynucleotides thereby generating said second database.

59. The system of claim 58, wherein said at least one sequence criterion for computationally selecting said at least a portion of said expressed polynucleotide is selected from the group consisting of sequence length, sequence annotation, sequence information, intron splice consensus site, intron sharing, sequence overlap, rare restriction site , poly(T) head, poly(A) tail, and poly(A) signal.

60. The system of claim 54 further comprising the step of testing the putative naturally occurring antisense transcripts for an ability to form said duplex with said at least one sense oriented polynucleotide sequence under physiological conditions.

61. The system of claim 54 further comprising the step of computationally testing the putative naturally occurring antisense transcripts according to at least one criterion selected from the group consisting of sequence annotation, sequence information, intron splice consensus site, intron sharing, sequence overlap, rare restriction site , poly(T) head, poly(A) tail, and poly(A) signal.

62. A method of identifying putative naturally occurring antisense transcripts, the method comprising screening a database of expressed polynucleotides sequences according to at least one sequence criterion, said at least one sequence criterion being selected to identify putative naturally occurring antisense transcripts.

63. The method of claim 62, wherein said database includes sequences of a type selected from the group consisting of expressed sequence tags, contigs, complementary DNA (cDNA) sequences, pre-messenger RNA (mRNA) sequences and mRNA sequences.

64. The method of claim 62, wherein an average sequence length of said expressed polynucleotide sequences of said second database is selected from a range of 0.02 to 0.8 Kb.

65. The method of claim 62, wherein said at least one sequence criterion is selected from the group consisting of sequence length, sequence annotation, sequence information, intron splice consensus site, intron sharing, sequence overlap, rare restriction site , poly(T) head, poly(A) tail, and poly(A) signal.

66. The method of claim 62 further comprising the step of testing the putative naturally occurring antisense transcripts for an ability to form a duplex with at least one sense oriented polynucleotide sequence under physiological conditions.

67. A method of quantifying at least one mRNA of interest in a biological sample, the method comprising:

(a) contacting the biological sample with at least one oligonucleotide capable of binding with the at least one mRNA of interest, wherein said at least one oligonucleotide is designed and configured so as to be complementary to a sequence region of the mRNA transcript of interest, said sequence region not being complementary with a naturally occurring antisense transcript; and

(b) detecting a level of binding between the at least one mRNA of interest and said at least one oligonucleotide to thereby quantify the at least one mRNA of interest in the biological sample.

68. The method of claim 67, wherein said at least one oligonucleotide is attached to a solid substrate.

69. The method of claim 68, wherein said solid substrate is configured as a microarray and whereas said at least one oligonucleotide includes a plurality of oligonucleotides each attached to said microarray in a regio-specific manner.

70. The method of claim 67, wherein said at least one oligonucleotide is labeled and whereas step (b) is effected by quantifying said label.

WHAT IS CLAIMED IS:

1. A method of identifying putative naturally occurring antisense transcripts, the method comprising:

(a) computationally aligning a first database including sense-oriented polynucleotide sequences with a second database including expressed polynucleotide sequences; and

(b) identifying expressed polynucleotide sequences from said second database being capable of forming a duplex with at least one sense-oriented polynucleotide sequence of said first database, thereby identifying putative naturally occurring antisense transcripts.

2. The method of claim 1, wherein said first database includes sequences of a type selected from the group consisting of genomic sequences, expressed sequence tags, contigs, intron sequences, complementary DNA (cDNA) sequences, pre-messenger RNA (mRNA) sequences and mRNA sequences.

3. The method of claim 1, wherein said second database includes sequences of a type selected from the group consisting of expressed sequence tags, contigs, complementary DNA (cDNA) sequences, pre-messenger RNA (mRNA) sequences and mRNA sequences.

4. The method of claim 1, wherein an average sequence length of said expressed polynucleotide sequences of said second database is selected from a range of 0.02 to 0.8 Kb.

5. The method of claim 1, wherein said second database is generated by:

(i) providing a library of expressed polynucleotides;

(ii) obtaining sequence information of said expressed polynucleotides;

(iii) computationally selecting at least a portion of said expressed polynucleotides according to at least one sequence criterion; and

(iv) storing said sequence information of said at least a portion of said expressed polynucleotides thereby generating said second database.

6. The method of claim 5, wherein said at least one sequence criterion for computationally selecting said at least a portion of said expressed polynucleotide is selected from the group consisting of sequence length, sequence annotation, sequence information, intron splice consensus site, intron sharing, sequence overlap, rare restriction site, poly(T) head, poly(A) tail, and poly(A) signal.

7. The method of claim 1 further comprising the step of testing the putative naturally occurring antisense transcripts for an ability to form said duplex with said at least one sense oriented polynucleotide sequence under physiological conditions.

8. The method of claim 1 further comprising the step of computationally testing the putative naturally occurring antisense transcripts according to at least one criterion selected from the group consisting of sequence annotation, sequence information, intron splice consensus site, intron sharing, sequence overlap, rare restriction site, poly(T) head, poly(A) tail, and poly(A) signal.

9. A kit for quantifying at least one mRNA transcript of interest, the kit comprising at least one oligonucleotide being designed and configured so as to be complementary to a sequence region of the mRNA transcript of interest, said sequence region not being complementary with a naturally occurring antisense transcript.

10. The kit of claim 9, wherein a length of said at least one oligonucleotide is selected from a range of 15-200 nucleotides.

11. The kit of claim 9, wherein said at least one oligonucleotide is a single stranded oligonucleotide.

12. The kit of claim 9, wherein said at least one oligonucleotide is a double stranded oligonucleotide.

13. The kit of claim 9, wherein a guanidine and cytosine content of said at least one oligonucleotide is at least 25 %.

14. The kit of claim 9, wherein said at least one oligonucleotide is labeled.

15. The kit of claim 9, wherein said at least one oligonucleotide is attached to a solid substrate.

16. The kit of claim 15, wherein said solid substrate is configured as a microarray and whereas said at least one oligonucleotide includes a plurality of oligonucleotides each attached to said microarray in a regio-specific manner.

17. A kit for quantifying at least one mRNA transcript of interest, the kit comprising at least one pair of oligonucleotides including a first oligonucleotide capable of binding the at least one mRNA transcript of interest and a second oligonucleotide being capable of binding a naturally occurring antisense transcript complementary to the mRNA of interest.

18. The kit of claim 17, wherein a length of each of said first and second oligonucleotides is selected from a range of 15-200 nucleotides

19. The kit of claim 17, wherein said first and second oligonucleotides are single stranded oligonucleotides.

20. The kit of claim 17, wherein said first and second oligonucleotides are double stranded oligonucleotide.

21. The kit of claim 17, wherein a guanidine and cytosine content of each of said first and second oligonucleotides is at least 25 %.

22. The kit of claim 17, wherein said first and second oligonucleotides are labeled.

23. The kit of claim 17, wherein said first and second oligonucleotides are attached to a solid substrate.

24. The kit of claim 23, wherein said solid substrate is configured as a microarray and whereas each of said first and second oligonucleotides includes a plurality of oligonucleotides each attached to said microarray in a regio-specific manner.

25. A kit for quantifying at least one naturally occurring antisense transcript of interest, the kit comprising at least one oligonucleotide being designed and configured so as to be complementary to a sequence region of the at least one naturally occurring antisense transcript of interest, said sequence region not being complementary with a naturally occurring mRNA transcript.

26. The kit of claim 25, wherein a length of said at least one oligonucleotide is selected from a range of 15-200 nucleotides.

27. The kit of claim 25, wherein said at least one oligonucleotide is a single stranded oligonucleotide.

28. The kit of claim 25, wherein said at least one oligonucleotide is a double stranded oligonucleotide.

29. The kit of claim 25, wherein a guanidine and cytosine content of said at least one oligonucleotide is at least 25 %.

30. The kit of claim 25, wherein said at least one oligonucleotide is labeled.

31. The kit of claim 25, wherein said at least one oligonucleotide is attached to a solid substrate.

32. The kit of claim 31, wherein said solid substrate is configured as a microarray and whereas said at least one oligonucleotide includes a plurality of oligonucleotides each attached to said microarray in a regio-specific manner.

33. A method of designing artificial antisense transcripts, the method comprising:

(a) providing a database of naturally occurring antisense transcripts;

(b) extracting from said database criteria governing structure and/or function of said naturally occurring antisense transcripts; and

(c) designing the artificial antisense transcripts according to said criteria.

34. The method of claim 33, wherein said criteria governing structure and/or function of said naturally occurring antisense transcripts are selected from the group consisting of antisense length, complementarity length, complementarity position, intron molecules, alternative splicing sites, tissue specificity, pathological abundance, chromosomal mapping, open reading frames, promoters, hairpin structures, helix structures, stem and loops, pseudoknots and tertiary interactions, guanidine and/or cytosine content, guanidine tandems, adenosine content, thermodynamic criteria, RNA duplex melting point, RNA modifications, protein-binding motifs, palindromic sequence and predicted single stranded and double stranded regions.

35. The method of claim 33, wherein said step of providing said database of naturally occurring antisense transcripts is effected by:

(a) computationally aligning a first database including sense-oriented polynucleotide sequences with a second database including expressed polynucleotide sequences; and

(b) identifying expressed polynucleotide sequences from said second database being capable of forming a duplex with at least one sense-oriented polynucleotide sequence of said first database,

(c) storing a sequence. of said expressed polynucleotide sequences identified in step (b), thereby providing said database of said naturally occurring antisense transcripts..

36. The method of claim 35, wherein said first database includes sequences of a type selected from the group consisting of genomic sequences, expressed sequence tags, contigs, intron sequences, complementary DNA (cDNA) sequences, pre-messenger RNA (mRNA) sequences and mRNA sequences.

37. The method of claim 35, wherein said second database includes sequences of a type selected from the group consisting of expressed sequence tags, contigs, complementary DNA (cDNA) sequences, pre-messenger RNA (mRNA) sequences and mRNA sequences.

38. The method of claim 35, wherein an average sequence length of said expressed polynucleotide sequences of said second database is selected from a range of 0.02 to 0.8 Kb.

39. The method of claim 35, wherein said second database is generated by:

(i) providing a library of expressed polynucleotides;

(ii) obtaining sequence information of said expressed polynucleotides;

(iii) computationally selecting at least a portion of said expressed polynucleotides according to at least one sequence criterion; and

(iv) storing said sequence information of said at least a portion of said expressed polynucleotides thereby generating said second database.

40. The method of claim 39, wherein said at least one sequence criterion for computationally selecting said at least a portion of said expressed polynucleotide is selected from the group consisting of sequence length, sequence annotation,

sequence information, intron splice consensus site, intron sharing, sequence overlap, rare restriction site , poly(T) head, poly(A) tail, and poly(A) signal.

41. The method of claim 35, further comprising the step of testing said putative naturally occurring antisense transcripts for an ability to form said duplex with said at least one sense oriented polynucleotide sequence under physiological conditions.

42. The method of claim 35 further comprising the step of computationally testing said putative naturally occurring antisense transcripts according to at least one criterion selected from the group consisting of sequence annotation, sequence information, intron splice consensus site, intron sharing, sequence overlap, rare restriction site , poly(T) head, poly(A) tail, and poly(A) signal.

43. A computer readable storage medium comprising a database including a plurality of sequences, wherein each sequence is of a naturally occurring antisense transcript.

44. The computer readable storage medium of claim 43, wherein said database further includes information pertaining to each sequence of said naturally occurring antisense transcripts, said information is selected from the group consisting of related sense gene, antisense length, complementarity length, complementarity position, intron molecules, alternative splicing sites, tissue specificity, pathological abundance, chromosomal mapping, open reading frames, promoters, hairpin structures, helix structures, stem and loops, pseudoknots and tertiary interactions, guanidine and/or cytosine content, guanidine tandems, adenosine content, thermodynamic criteria, RNA duplex melting point, RNA modifications, protein-binding motifs, palindromic sequence and predicted single stranded and double stranded regions.

45. The computer readable storage medium of claim 43, wherein said database further includes information pertaining to generation of said database and potential uses of said database.

46. A method of generating a database of naturally occurring antisense transcripts, the method comprising:

(a) computationally aligning a first database including sense-oriented polynucleotide sequences with a second database including expressed polynucleotide sequences;

(b) identifying expressed polynucleotide sequences from said second database being capable of forming a duplex with at least one sense-oriented polynucleotide sequence of said first database so as to identify putative naturally occurring antisense transcripts; and

(c) storing sequence information of said identified naturally occurring antisense transcripts, thereby generating the database of the naturally occurring antisense transcripts.

47. The method of claim 46, wherein the database is set forth in the file seqs_125 and/or seqs_133 of the enclosed CD-ROM1, alignments_125, table_125, Table_S1 and/or Table_S2 of the enclosed CD-ROM2, alignments_133 and/or table_133 of the enclosed CD-ROM3, alignments_136, mouse_alignments, mouse_seqs, mouse_table, nuc_seqs_136, orthology, pep_seqs_136, table_136, annotations_136 and/or antisense of the enclosed CD-ROM4.

48. The method of claim 46, wherein said first database includes sequences of a type selected from the group consisting of genomic sequences, expressed sequence tags, contigs, intron sequences, complementary DNA (cDNA) sequences, pre-messenger RNA (mRNA) sequences and mRNA sequences.

49. The method of claim 46, wherein said second database includes sequences of a type selected from the group consisting of expressed sequence tags,

contigs, complementary DNA (cDNA) sequences, pre-messenger RNA (mRNA) sequences and mRNA sequences.

50. The method of claim 46, wherein an average sequence length of said expressed polynucleotide sequences of said second database is selected from a range of 0.02 to 0.8 Kb.

51. The method of claim 46, wherein said second database is generated by:

(i) providing a library of expressed polynucleotides;

(ii) obtaining sequence information of said expressed polynucleotides;

(iii) computationally selecting at least a portion of said expressed polynucleotides according to at least one sequence criterion; and

(iv) storing said sequence information of said at least a portion of said expressed polynucleotides thereby generating said second database.

52. The method of claim 51, wherein said at least one sequence criterion for computationally selecting said at least a portion of said expressed polynucleotide is selected from the group consisting of sequence length, sequence annotation, sequence information, intron splice consensus site, intron sharing, sequence overlap, rare restriction site , poly(T) head, poly(A) tail, and poly(A) signal.

53. The method of claim 46 further comprising the step of testing the putative naturally occurring antisense transcripts for an ability to form said duplex with said at least one sense oriented polynucleotide sequence under physiological conditions.

54. The method of claim 46 further comprising the step of computationally testing the putative naturally occurring antisense transcripts according to at least one criterion selected from the group consisting of sequence annotation, sequence information, intron splice consensus site, intron sharing, sequence overlap, rare restriction site , poly(T) head, poly(A) tail, and poly(A) signal.

55. A system for generating a database of a plurality of putative naturally occurring antisense transcripts, the system comprising a processing unit, said processing unit executing a software application configured for:

(a) computationally aligning a first database including sense-oriented polynucleotide sequences with a second database including expressed polynucleotide sequences; and

(b) identifying expressed polynucleotide sequences from said second database being capable of forming a duplex with at least one sense-oriented polynucleotide sequence of said first database.

56. The system of claim 55, wherein said first database includes sequences of a type selected from the group consisting of genomic sequences, expressed sequence tags, contigs, intron sequences, complementary DNA (cDNA) sequences, pre-messenger RNA (mRNA) sequences and mRNA sequences.

57. The system of claim 55, wherein said second database includes sequences of a type selected from the group consisting of expressed sequence tags, contigs, complementary DNA (cDNA) sequences, pre-messenger RNA (mRNA) sequences and mRNA sequences.

58. The system of claim 55, wherein an average sequence length of said expressed polynucleotide sequences of said second database is selected from a range of 0.02 to 0.8 Kb.

59. The system of claim 55, wherein said second database is generated by:

(i) providing a library of expressed polynucleotides;

(ii) obtaining sequence information of said expressed polynucleotides;

(iii) computationally selecting at least a portion of said expressed polynucleotides according to at least one sequence criterion; and

(iv) storing said sequence information of said at least a portion of said expressed polynucleotides thereby generating said second database.

60. The system of claim 59, wherein said at least one sequence criterion for computationally selecting said at least a portion of said expressed polynucleotide is selected from the group consisting of sequence length, sequence annotation, sequence information, intron splice consensus site, intron sharing, sequence overlap, rare restriction site , poly(T) head, poly(A) tail, and poly(A) signal.

61. The system of claim 55 further comprising the step of testing the putative naturally occurring antisense transcripts for an ability to form said duplex with said at least one sense oriented polynucleotide sequence under physiological conditions.

62. The system of claim 55 further comprising the step of computationally testing the putative naturally occurring antisense transcripts according to at least one criterion selected from the group consisting of sequence annotation, sequence information, intron splice consensus site, intron sharing, sequence overlap, rare restriction site , poly(T) head, poly(A) tail, and poly(A) signal.

63. A method of identifying putative naturally occurring antisense transcripts, the method comprising screening a database of expressed polynucleotides sequences according to at least one sequence criterion, said at least one sequence criterion being selected to identify putative naturally occurring antisense transcripts.

64. The method of claim 63, wherein said database includes sequences of a type selected from the group consisting of expressed sequence tags, contigs, complementary DNA (cDNA) sequences, pre-messenger RNA (mRNA) sequences and mRNA sequences.

65. The method of claim 63, wherein an average sequence length of said expressed polynucleotide sequences of said second database is selected from a range of 0.02 to 0.8 Kb.

66. The method of claim 63, wherein said at least one sequence criterion is selected from the group consisting of sequence length, sequence annotation, sequence information, intron splice consensus site, intron sharing, sequence overlap, rare restriction site , poly(T) head, poly(A) tail, and poly(A) signal.

67. The method of claim 63 further comprising the step of testing the putative naturally occurring antisense transcripts for an ability to form a duplex with at least one sense oriented polynucleotide sequence under physiological conditions.

68. A method of quantifying at least one mRNA of interest in a biological sample, the method comprising:

(a) contacting the biological sample with at least one oligonucleotide capable of binding with the at least one mRNA of interest, wherein said at least one oligonucleotide is designed and configured so as to be complementary to a sequence region of the mRNA transcript of interest, said sequence region not being complementary with a naturally occurring antisense transcript; and

(b) detecting a level of binding between the at least one mRNA of interest and said at least one oligonucleotide to thereby quantify the at least one mRNA of interest in the biological sample.

69. The method of claim 68, wherein said at least one oligonucleotide is attached to a solid substrate.

70. The method of claim 69, wherein said solid substrate is configured as a microarray and whereas said at least one oligonucleotide includes a plurality of oligonucleotides each attached to said microarray in a regio-specific manner.

71. The method of claim 68, wherein said at least one oligonucleotide is labeled and whereas step (b) is effected by quantifying said label.

72. The method of claim 68, wherein a length of said at least one oligonucleotide is selected from a range of 15-200 nucleotides.

73. The method of claim 68, wherein said at least one oligonucleotide is a single stranded oligonucleotide.

74. The method of claim 68, wherein said at least one oligonucleotide is a double stranded oligonucleotide.

75. The method of claim 68, wherein a guanidine and cytosine content of said at least one oligonucleotide is at least 25 %.

76. A method of quantifying the expression potential of at least one mRNA of interest in a biological sample, the method comprising:

(a) contacting the biological sample with at least one pair of oligonucleotides including a first oligonucleotide capable of binding the at least one mRNA of interest and a second oligonucleotide being capable of binding a naturally occurring antisense transcript complementary to the mRNA of interest; and

(b) detecting a level of binding between the at least one mRNA of interest and said first oligonucleotide and a level of binding between said naturally occurring antisense transcript complementary to the mRNA of interest and said second oligonucleotide to thereby quantify the expression potential of the at least one mRNA of interest in the biological sample.

77. The method of claim 76, wherein a length of each of said first and second oligonucleotides is selected from a range of 15-200 nucleotides

78. The method of claim 76, wherein said first and second oligonucleotides are single stranded oligonucleotides.

79. The method of claim 76, wherein said first and second oligonucleotides are double stranded oligonucleotide.

80. The method of claim 76, wherein a guanidine and cytosine content of each of said first and second oligonucleotides is at least 25 %.

81. The method of claim 76, wherein said first and second oligonucleotides are labeled and whereas step (b) is effected by quantifying said label.

82. The method of claim 76, wherein said first and second oligonucleotides are attached to a solid substrate.

83. The method of claim 82, wherein said solid substrate is configured as a microarray and whereas each of said first and second oligonucleotides includes a plurality of oligonucleotides each attached to said microarray in a regio-specific manner.

84. A method of quantifying at least one naturally occurring antisense transcript of interest in a biological sample, the method comprising:

(a) contacting the biological sample with at least one oligonucleotide capable of binding with the at least one naturally occurring antisense transcript of interest, wherein said at least one oligonucleotide is designed and configured so as to be complementary to a sequence region of the naturally occurring antisense transcript of interest, said sequence region not being complementary with a naturally occurring mRNA transcript; and

(b) detecting a level of binding between the at least one naturally occurring antisense transcript of interest and said at least one oligonucleotide to thereby quantify the at least one naturally occurring antisense transcript of interest in the biological sample.

85. The method of claim 84, wherein said at least one oligonucleotide is attached to a solid substrate.

86. The method of claim 85, wherein said solid substrate is configured as a microarray and whereas said at least one oligonucleotide includes a plurality of oligonucleotides each attached to said microarray in a regio-specific manner.

87. The method of claim 84, wherein said at least one oligonucleotide is labeled and whereas step (b) is effected by quantifying said label.

88. The method of claim 84, wherein a length of said at least one oligonucleotide is selected from a range of 15-200 nucleotides.

89. The method of claim 84, wherein said at least one oligonucleotide is a single stranded oligonucleotide.

90. The method of claim 84, wherein said at least one oligonucleotide is a double stranded oligonucleotide.

91. The method of claim 84, wherein a guanidine and cytosine content of said at least one oligonucleotide is at least 25 %.

92. A method of identifying a novel drug target, the method comprising:

(a) determining expression level of at least one naturally occurring antisense transcript of interest in cells characterized by an abnormal phenotype; and

(b) comparing said expression level of said at least one naturally occurring antisense transcript of interest in said cells characterized by an abnormal phenotype to an expression level of said at least one naturally occurring antisense transcript of interest in cells characterized by a normal phenotype, to thereby identify the novel drug target.

93. The method of claim 92, wherein said abnormal phenotype of said cells is selected from the group consisting of biochemical phenotype, morphological phenotype and nutritional phenotype.

94. The method of claim 92, wherein said determining expression level of at least one naturally occurring antisense transcript of interest is effected by at least one oligonucleotide designed and configured so as to be complementary to a sequence region of said at least one naturally occurring antisense transcript of interest, said sequence region not being complementary with a naturally occurring mRNA transcript.

95. The method of claim 94, wherein a length of said at least one oligonucleotide is selected from a range of 15-200 nucleotides.

96. The method of claim 94, wherein said at least one oligonucleotide is a single stranded oligonucleotide.

97. The method of claim 94, wherein said at least one oligonucleotide is a double stranded oligonucleotide.

98. The method of claim 94, wherein a guanidine and cytosine content of said at least one oligonucleotide is at least 25 %.

99. The method of claim 94, wherein said at least one oligonucleotide is labeled and whereas step (b) is effected by quantifying said label.

100. The method of claim 94, wherein said at least one oligonucleotide is attached to a solid substrate.

101. The method of claim 100, wherein said solid substrate is configured as a microarray and whereas said at least one oligonucleotide includes a plurality of oligonucleotides each attached to said microarray in a regio-specific manner.

102. A method of treating or preventing a disease, condition or syndrome associated with an upregulation of a naturally occurring antisense transcript complementary to a naturally occurring mRNA transcript, the method comprising administering a therapeutically effective amount of an agent for regulating expression of the naturally occurring antisense transcript.

103. The method of claim 102, wherein said agent for regulating expression of the naturally occurring antisense transcript is at least one oligonucleotide designed and configured so as to hybridize to a sequence region of said at least one naturally occurring antisense transcript.

104. The method of claim 103, wherein said at least one oligonucleotide is a ribozyme.

105. The method of claim 103, wherein said at least one oligonucleotide is a sense transcript.

106. A method of diagnosing a disease, condition or syndrome associated with a substandard expression ratio of an mRNA of interest over a naturally occurring antisense transcript complementary to the mRNA of interest, the method comprising:

(a) quantifying expression level of the mRNA of interest and the naturally occurring antisense transcript complementary to the mRNA of interest;

(b) calculating the expression ratio of the mRNA of interest over the naturally occurring antisense transcript complementary to the mRNA of interest, thereby diagnosing the disease, condition or syndrome.

107. The method of claim 106, wherein quantifying said expression level of the mRNA of interest and the naturally occurring antisense transcript complementary to the mRNA of interest is effected by at least one pair of oligonucleotides including a first oligonucleotide capable of binding the mRNA of interest and a second oligonucleotide being capable of binding the naturally occurring antisense transcript complementary to the mRNA of interest.

108. The method of claim 107, wherein a length of each of said first and second oligonucleotides is selected from a range of 15-200 nucleotides

109. The method of claim 107, wherein said first and second oligonucleotides are single stranded oligonucleotides.

110. The method of claim 107, wherein said first and second oligonucleotides are double stranded oligonucleotides.

111. The method of claim 107, wherein a guanidine and cytosine content of each of said first and second oligonucleotides is at least 25 %.

112. The method of claim 107, wherein said first and second oligonucleotides are labeled.

113. The method of claim 107, wherein said first and second oligonucleotides are attached to a solid substrate.

114. The method of claim 113, wherein said solid substrate is configured as a microarray and whereas each of said first and second oligonucleotides includes a plurality of oligonucleotides each attached to said microarray in a regio-specific manner.

115. A method of identifying co-regulated human polynucleotide sequences , the method comprising:

(a) computationally identifying non-human polynucleotide sequence pairs, each corresponding to an mRNA sequence and its naturally occurring antisense transcript;

(b) computationally identifying for each polynucleotide sequence of said polynucleotide sequence pairs a human orthologue polynucleotide sequence, thereby identifying human polynucleotide sequence pairs; and

(c) selecting from said human polynucleotide sequence pairs, specific polynucleotide sequence pairs having oppositely oriented polynucleotide sequences which are localized to a chromosome region, said specific polynucleotide sequence pairs being co-regulated human polynucleotide sequences.

116. The method of claim 115, wherein said specific polynucleotide sequence pairs are gapped by a distance not exceeding a predetermined value.

117. The method of claim 116, wherein said predetermined value does not exceed 10 Kb.

118. The method of claim 115, wherein step (a) is effected by:

(a) computationally aligning a first database including sense-oriented polynucleotide sequences with a second database including expressed polynucleotide sequences; and

(b) identifying expressed polynucleotide sequences from said second database being capable of forming a duplex with at least one sense-oriented polynucleotide sequence of said first database, thereby identifying said polynucleotide sequence pairs of mRNA sequences and naturally occurring antisense transcripts complementary to the mRNA sequences.

119. The method of claim 115, wherein step (b) is effected by a homology screening software application.

120. The method of claim 115, further comprising identifying oppositely oriented expressed sequences corresponding to the human co-regulated polynucleotide sequences.

121. A system for generating a database of co-regulated human polynucleotide sequences, the system comprising a processing unit, said processing unit executing a software application configured for:

(a) computationally identifying non-human polynucleotide sequence pairs, each corresponding to an mRNA sequence and its naturally occurring antisense transcript;

(b) computationally identifying for each polynucleotide sequence of said polynucleotide sequence pairs a human orthologue polynucleotide sequence, thereby identifying human polynucleotide sequence pairs;

(c) selecting from said human polynucleotide sequence pairs, specific polynucleotide sequence pairs having oppositely oriented polynucleotide sequences which are localized to a chromosome region, said specific polynucleotide sequence pairs being co-regulated human polynucleotide sequences; and

(d) storing the co-regulated human polynucleotide sequences to therevy generate the database of co-regulated human polynucleotide sequences

122. The system of claim 121, wherein said specific polynucleotide sequence pairs are gapped by a distance not exceeding a predetermined value.

123. The system of claim 122, wherein said predetermined value does not exceed 10 Kb.

124. The system of claim 121, wherein step (a) is effected by:

(a) computationally aligning a first database including sense-oriented polynucleotide sequences with a second database including expressed polynucleotide sequences; and

(b) identifying expressed polynucleotide sequences from said second database being capable of forming a duplex with at least one sense-oriented polynucleotide sequence of said first database, thereby identifying said polynucleotide sequence pairs of mRNA sequences and naturally occurring antisense transcripts complementary to the mRNA sequences.

125. The system of claim 121, wherein step (b) is effected by a homology screening software application.

126. The system of claim 121, further comprising identifying oppositely oriented expressed sequences corresponding to the human co-regulated polynucleotide sequences.

127. A computer readable storage medium comprising data stored in a retrievable manner, said data including sequence information of co-regulated human polynucleotide sequences as set forth in files seqs_125 and/or seqs_133 of enclosed CD-1, mouse_seqs, nuc_seqs_136 and/or pep_seqs_136 of enclosed CD-ROM4 and sequence annotations as set forth in the file annotations_136 of enclosed CD-ROM4.

128. A method of modulating an activity or expression of a gene product, the method comprising upregulating or down regulating expression or activity of a naturally occurring antisense transcript of the gene product, thereby modulating the activity or expression of the gene product.

129. The method of claim 128, further comprising upregulating or down regulating expression or activity of the gene product.

130. An isolated polynucleotide comprising any of the nucleic acid sequences set forth in the file seqs_125 or seqs_133 of the enclosed CD-ROM1; or in the file nuc_seqs_136 of the enclosed CD-ROMs 1-4.

131. An isolated polypeptide comprising any of the amino acid sequences set forth in the file pep_seqs_136 of enclosed CD-ROM4.